

In this issue

High resolution map of the bovine hornless locus

The hornless phenotype in cattle is of interest due to its economic importance. **Cord Drögemüller *et al.*** have produced a 4 Mb high resolution BAC contig of the bovine chromosome 1q12 region which contains the putative locus and used it to refine the comparative map with human chromosome 21q22.

Cadherin repertoire of the mosquito, and comparison to the fruitfly

The cadherin superfamily is involved in cell-cell communication and adhesion and is widely represented across the evolutionary tree. **Catarina Moita and colleagues** have used a bioinformatic approach to identify the cadherin repertoire of *Anopheles gambiae* (the mosquito) and compared it to that of the fruitfly *Drosophila melanogaster*.

Phylogenomic analysis of the alphavirus genus

Using full or partial genome sequence data from alphavirus genomes **Aimée Luers and coworkers** have made a phylogenomic study of the alphavirus genus. Their approach, which uses much more data for each virus than prior studies, has yielded some novel insights into the evolution of this genus.

Special section of reviews and papers from the Plant and Animal Genomes XIII (PAGXIII) conference

Ulrik John and colleagues have termed their approach for identifying novel genes and alleles

from indigenous and exotic species Xenogenomics. This genomic bioprospecting involves EST discovery, cDNA microarray-based expression profiling and functional genomics and is being applied to indigenous Australian flora and native Antarctic plants.

Robert Moritz *et al.* describe their novel pre-fractionation strategy, which uses two-dimensional free-flow electrophoresis. This technique can fractionate large quantity protein samples and is applicable to both high- M_r proteins and small peptides. They have applied it to the proteomic analysis of colorectal cancer, to discover biomarkers for this disease.

Fatal bovine respiratory infections usually occur when a primary viral infection compromises host defences and enhances the severity of a secondary bacterial infection. **Paul Hodgson and colleagues** discuss their observations on the effect of stress on this viral-bacterial synergy, which appears to be enacted via regulation of inflammation.

Lawrence Schook and coworkers review the Swine Genome Sequencing Consortium (SGSC) workshop: A Strategic Roadmap for Sequencing the Pig Genome. Presentations reported the completion of a human-pig comparative map, and BAC fingerprint contigs for each of the autosomes and X chromosomes, which have been anchored using BLAST analysis and RH-mapping. Significant progress has been made towards the creation of a minimal tiling path for sequencing.

Conference Calendar

A listing of genomics related conferences planned for October to December 2005.